In the Specification:

On page 1, please amend the title as follows:

~~NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR~~
CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3)
ANTIBODIES

On page 1, please amend the "Related Applications" paragraph as follows:

This application is a divisional application of U.S. Patent Application Serial No.
09/757,982, filed January 10, 2001, now U.S. Patent 6,740,737, which is a divisional application
of U.S. Patent Application Serial No. 09/163,115, filed September 29, 1998, now U.S. Patent
6,183,962, which claims priority to U.S. provisional Application No. 60/099,657, filed on
September 9, 1998, abandoned, all of which are incorporated herein in their entirety by this
reference.

On page 33, please amend the paragraphs beginning at line 12 as follows:

The comparison of sequences and determination of percent identity between two
sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the
percent identity between two amino acid sequences is determined using the GAP program in the
GCG software package (available at http://www.gcg.com), using either a Blossom 62 matrix or a
PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5,
or 6. In yet another preferred embodiment, the percent identity between two nucleotide
sequences is determined using the GAP program in the GCG software package (available at
http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80
and a length weight of 1, 2, 3, 4, 5, or 6.

The nucleic acid and protein sequences of the present invention can further be used as a
"query sequence" to perform a search against public databases to, for example, identify other
family members or related sequences. Such searches can be performed using the NBLAST and
XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST
nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12
to obtain nucleotide sequences homologous to CSAPK nucleic acid molecules of the invention.
BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength =

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3 to obtain amino acid sequences homologous to CSAPK protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See ~~http://~~www.ncbi.nlm.nih.gov.

On page 118, please amend the title as follows:

~~NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR~~ <u>CARDIOVASCULAR SYSTEM ASSOCIATED PROTEIN KINASE 3 (CSAPK-3) ANTIBODIES</u>